

D. KRUSE

RECEIVED Page 1 of 7 #18
NOV 27 2003
TECH CENTER 1600/2900 1638

RAW SEQUENCE LISTING DATE: 11/07/2000
PATENT APPLICATION: US/08/945,144A TIME: 11:38:40

Input Set : A:\Rpmu5e.app
Output Set: N:\CRF3\11072000\H945144A.raw

3 <110> APPLICANT: Lebrun, Michel
4 Sailland, Alain
5 Freyssinet, Georges
6 DeGryse, Eric
8 <120> TITLE OF INVENTION: Mutated 5-Enol Pyruvylshikimate-3-Phosphate Synthase,
9 Gene Coding for Said Protein and Transformed Plants
10 Containing Said Gene
12 <130> FILE REFERENCE: 5500-13
14 <140> CURRENT APPLICATION NUMBER: 08/945,144A
15 <141> CURRENT FILING DATE: 1998-01-20
17 <150> PRIOR APPLICATION NUMBER: PCT/FR96/01125
18 <151> PRIOR FILING DATE: 1996-07-18
20 <150> PRIOR APPLICATION NUMBER: FRANCE 95/08979
21 <151> PRIOR FILING DATE: 1995-07-19
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: PatentIn Ver. 2.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1713
29 <212> TYPE: DNA
30 <213> ORGANISM: Zea mays
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37 ccatcaaggga gatctccggc accgtcaagc tgcgggggtc caagtcgctt tccaaccgga 180
39 tcctcctact cgcgcacctg tccgagggga caacagtggg tgataacctg ctgaacagtg 240
41 aggatgtcca ctacatgtc ggggccttga ggactcttgg tctctctgtc gaagcggaca 300
43 aagctgcccc aagagctgta gttgttggct gtgggtggaa gttcccgatt gaggatgcta 360
45 aagagggaag gcagctcttc ttgggggaatg ctggaactgc aatgcggcca ttgacagcag 420
47 ctgttactgc tgcgtgttga aatgcaactt acgtgcttga tggagtacca agaatgaggg 480
49 agagacccat tggcgacttg gttgtcggat tgaagcagct tgggtgcagat gttgattggt 540
51 tccttyggca tgactgcccc cctgttcgtg tcaatggaat cggagggcta cctggttgca 600
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55 ctlttygctct tggggatgtg gagattgaaa tcattgataa attaatctcc attccgtacg 720
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69 ctgatgtcgc calgactcct gctgtggttg cctcttttgc cgtatggccc acagccatca 1140
71 gagacgttgc ttccctggaga gtaaaaggaga ccgagaggat ggttgcgac cggacggagc 1200
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79 ccttccccga ctacttcgat gtgctgagca ctttctgcaa gaattataa agcgtgcgat 1440
81 actaccacgc agcttgattg aagtgatagg cttgtgtgta ggaatacat ttcttttgtt 1500
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85 tttctatttc ggaatcttaag tttgtgcact gtaagccaaa tttcatttca agagtgggttc 1620
87 gttggaataa taagaataat aaattacgtt tcagtgaataa aaaaaaaaaa aaaaaaaaaa 1680
89 aaaaaaaaaa aaaaaaaaaa aaccgggaa ttc 1713
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95 <213> ORGANISM: Zea mays
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99 <222> LOCATION: (6)..(1337)
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106 gcc acc gtc aag ctg ccg ggg tcc aag tgg ctt tcc aac cgg atc ctc 98
107 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
108 20 25 30
110 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146
111 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
112 35 40 45
114 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194
115 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
116 50 55 60
118 ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt gcc 242
119 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
120 65 70 75
122 tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc 290
123 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
124 80 85 90 95
126 ttc ttg ggg aat gct gga act gca atg cgg cca ttg aca gca gct gtt 338
127 Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val
128 100 105 110
130 act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga 386
131 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
132 115 120 125
134 atg agg gag aga ccc att gcc gac ttg gtt gtc gga ttg aag cag ctt 434
135 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
136 130 135 140
138 ggt gca gat gtt gat tgt ttc ctt gcc act gac tgc cca cct gtt cgt 482
139 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
140 145 150 155
142 gtc aat gga atc gga ggg cta cct ggt gcc aag gtc aag ctg tct gcc 530
143 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly
144 160 165 170 175
146 tcc atc agc agt cag tac ttg agt gcc ttg ctg atg gct gct cct ttg 578
147 Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu
148 180 185 190
150 gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att 626
151 Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile

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154 ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa 674
155 Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys
156          210          215          220
158 gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa 722
159 Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln
160          225          230          235
162 aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc 770
163 Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser
164 240          245          250          255
166 gca aqc tat ttc ttg gct ggt gct gca att act gga ggg act gtg act 818
167 Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr
168          260          265          270
170 gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct 866
171 Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala
172          275          280          285
174 gag gta ctg gag atg atg gga gcg aag gtt aca tgg acc gag act aqc 914
175 Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser
176          290          295          300
178 gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc 962
179 Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu
180          305          310          315
182 aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act 1010
183 Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr
184 320          325          330          335
186 ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac 1058
187 Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp
188          340          345          350
190 gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg 1106
191 Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg
192          355          360          365
194 acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg qac tac 1154
195 Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr
196          370          375          380
198 tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg 1202
199 Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr
200          385          390          395
202 tac gac gac cac agg atg gcc atg gcc ttc tcc ctt gcc gcc tgt gcc 1250
203 Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala
204 400          405          410          415
206 gag gtc ccc gtc acc atc ccg gac cct ggg tgc acc ccg aag acc ttc 1298
207 Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe
208          420          425          430
210 ccc gac tac ttc gat gtg ctg agc act ttc gtc aag aat taa 1340
211 Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
212          435          440
215 <210> SEQ ID NO: 3
216 <211> LENGTH: 444
217 <212> TYPE: PRT

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218 <213> ORGANISM: Zea mays
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227 Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
228 35 40 45
230 Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
231 50 55 60
233 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
234 65 70 75 80
236 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
237 85 90 95
239 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
240 100 105 110
242 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
243 115 120 125
245 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
246 130 135 140
248 Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
249 145 150 155 160
251 Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
252 165 170 175
254 Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
255 180 185 190
257 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
258 195 200 205
260 Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
261 210 215 220
263 Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
264 225 230 235 240
266 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
267 245 250 255
269 Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
270 260 265 270
272 Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
273 275 280 285
275 Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
276 290 295 300
278 Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
279 305 310 315 320
281 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
282 325 330 335
284 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
285 340 345 350
287 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
288 355 360 365
290 Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys

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293 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
294 385      390      395      400
296 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
297      405      410      415
299 Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
300      420      425      430
302 Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
303      435      440
306 <210> SEQ ID NO: 4
307 <211> LENGTH: 1340
308 <212> TYPE: DNA
309 <213> ORGANISM: Zea mays
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (6)..(1337)
315 <400> SEQUENCE: 4
316 ccattg gcc gcc gcc gag gag atc gtg ctg cag ccc atc aag gag atc tcc 50
317      Ala Gly Ala Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser
318      1      5      10      15
320 gcc acc gtc aag ctg ccg ggg tcc aag tcc ctt tcc aac cgg atc ctc 98
321 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
322      20      25      30
324 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146
325 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
326      35      40      45
328 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194
329 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
330      50      55      60
332 ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc 242
333 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
334      65      70      75
336 tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc 290
337 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
338 80      85      90      95
340 ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt 338
341 Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val
342      100      105      110
344 act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga 386
345 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
346      115      120      125
348 atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt 434
349 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
350      130      135      140
352 ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt 482
353 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
354      145      150      155
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357 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly

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VERIFICATION SUMMARY DATE: 11/07/2000
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